IN THE CLAIMS:

The claims have been amended as follows:

B2

1. (Currently Amended) ~~An~~ <u>An isolated</u> trehalose synthase protein <u>comprising the amino acid sequence as recited in SEQ ID NO: 2</u> ~~with the following amino acid sequence:~~

~~Met   Ser   Ile   Pro   Asp   Asn   Thr   Tyr   Ile   Glu   Trp   Leu   Val~~
~~   Ser   Gln~~
~~   5   10~~
~~   15~~
~~Ser   Met   Leu   His   Ala   Ala   Arg   Glu   Arg   Ser   Arg   His   Tyr~~
~~   Ala   Gly~~
~~   20   25~~
~~   30~~
~~Gln   Ala   Arg   Leu   Trp   Gln   Arg   Pro   Try   Ala   Gln   Ala   Arg~~
~~   Pro   Arg~~
~~   35   40~~
~~   45~~
~~Asp   Ala   Ser   Ala   Ile   Ala   Ser   Val   Trp   Phe   Thr   Ala   Tyr~~
~~   Pro   Ala~~
~~   50   55~~
~~   60~~
~~Ala   Ile   Ile   Thr   Pro   Glu   Gly   Gly   Thr   Val   Leu   Glu   Ala~~
~~   Leu   Gly~~
~~   65   70~~
~~   75~~
~~Asp   Asp   Arg   Leu   Trp   Ser   Ala   Leu   Ser   Glu   Leu   Gly   Val~~
~~   Gln   Gly~~
~~   80   85~~
~~   90~~
~~Ile   His   Asn   Gly   Pro   Met   Lys   Arg   Ser   Gly   Gly   Leu   Arg~~
~~   Gly   Arg~~
~~   95   100~~
~~   105~~
~~Glu   Phe   Thr   Pro   Thr   Ile   Asp   Gly   Asn   Phe   Asp   Arg   Ile~~
~~   Ser   Phe~~
~~   110   115~~
~~   120~~
~~Asp   Ile   Asp   Pro   Ser   Leu   Gly   Thr   Glu   Glu   Gln   Met   Leu~~
~~   Gln   Leu~~
~~   125   130~~
~~   135~~
~~Ser   Arg   Val   Ala   Ala   Ala   His   Asn   Ala   Ile   Val   Ile   Asp~~
~~   Asp   Ile~~
~~   140   145~~
~~   150~~
~~Val   Pro   Ala   His   Thr   Gly   Lys   Gly   Ala   Asp   Phe   Arg   Leu~~
~~   Ala   Glu~~
~~   155   160~~
~~   165~~
~~Met   Ala   Tyr   Gly   Asp   Tyr   Pro   Gly   Leu   Tyr   His   Met   Val~~
~~   Glu   Ile~~
~~   170   175~~

3

Cont
B2

180
| Arg | Glu | Glu | Asp | Trp | Glu | Leu | Leu | Pro | Glu | Val | Pro | Ala |
| | Gly | Arg | | | | | | | | | | |

185   190

195
| Asp | Ser | Val | Asn | Leu | Leu | Pro | Pro | Val | Val | Asp | Arg | Leu |
| | Lys | Glu | | | | | | | | | | |

200   205

210
| Lys | His | Tyr | Ile | Val | Gly | Gln | Leu | Gln | Arg | Val | Ile | Phe |
| | Phe | Glu | | | | | | | | | | |

215   220

225
| Pro | Gly | Ile | Lys | Asp | Thr | Asp | Trp | Ser | Val | Thr | Gly | Glu |
| | Val | Thr | | | | | | | | | | |

230   235

240
| Gly | Val | Asp | Gly | Lys | Val | Arg | Arg | Trp | Val | Tyr | Leu | His |
| | Tyr | Phe | | | | | | | | | | |

245   250

255
| Lys | Glu | Gly | Gln | Pro | Ser | Lue | Asn | Trp | Leu | Asp | Pro | Thr |
| | Phe | Ala | | | | | | | | | | |

260   265

270
| Ala | Gln | Gln | Leu | Ile | Ile | Gly | Asp | Ala | Leu | His | Ala | Ile |
| | Asp | Val | | | | | | | | | | |

275   280

285
| Thr | Gly | Ala | Arg | Val | Leu | Arg | Leu | Asp | Ala | Asn | Gly | Phe |
| | Leu | Gly | | | | | | | | | | |

290   295

300
| Val | Glu | Arg | Arg | Ala | Glu | Gly | Thr | Ala | Trp | Ser | Glu | Gly |
| | His | Pro | | | | | | | | | | |

305   310

315
| Leu | Ser | Val | Thr | Gly | Asn | Gln | Leu | Leu | Ala | Gly | Ala | Ile |
| | Arg | Lys | | | | | | | | | | |

320   325

330
| Ala | Gly | Gly | Phe | Ser | Phe | Gln | Glu | Leu | Asn | Leu | Thr | Ile |
| | Asp | Asp | | | | | | | | | | |

335   340

345
| Ile | Ala | Ala | Met | Ser | His | Gly | Gly | Ala | Asp | Leu | Ser | Tyr |
| | Asp | Phe | | | | | | | | | | |

350   355

360
| Ile | Thr | Arg | Pro | Ala | Tyr | His | His | Ala | Leu | Leu | Thr | Gly |
| | Asp | Thr | | | | | | | | | | |

365   370

375
| Glu | Phe | Leu | Arg | Met | Met | Leu | Arg | Glu | Val | His | Ala | Phe |
| | Gly | Ile | | | | | | | | | | |

380   385

390

Cont B2

Asp Pro Ala Ser Leu Ile His Ala Leu Gln Asn His Asp
   Glu Leu
395 400
405
Thr Leu Glu Leu Val His Phe Trp Thr Leu His Ala Tyr
   Asp His
410 415
420
Tyr His Tyr Lys Gly Gln Thr Leu Pro Gly Gly His Leu
   Arg Glu
425 430
435
His Ile Arg Glu Glu Met Tyr Glu Arg Leu Thr Gly Glu
   His Ala
440 445
450
Pro Tyr Asn Leu Lys Phe Val Thr Asn Gly Val Ser Cys
   Thr Thr
455 460
465
Ala Ser Val Ile Ala Ala Ala Leu Asn Ile Arg Asp Leu
   Asp Ala
470 475
480
Ile Gly Pro Ala Glu Val Glu Gln Ile Gln Arg Leu His
   Ile Leu
485 490
495
Leu Val Met Phe Asn Ala Met Gln Pro Gly Val Phe Ala
   Leu Ser
500 505
510
Gly Trp Asp Leu Val Gly Ala Leu Pro Leu Ala Pro Glu
   Gln Val
515 520
525
Glu His Leu Met Gly Asp Gly Asp Thr Arg Trp Ile Asn
   Arg Gly
530 535
540
Gly Tyr Asp Leu Ala Asp Leu Ala Pro Glu Ala Ser Val
   Ser Ala
545 550
555
Glu Gly Leu Pro Lys Ala Arg Ser Leu Tyr Gly Ser Leu
   Ala Glu
560 565
570
Gln Leu Gln Arg Pro Gly Ser Phe Ala Cys Gln Leu Lys
   Arg Ile
575 580
585
Leu Ser Val Arg Gln Ala Tyr Asp Ile Ala Ala Ser Lys
   Gln Ile
590 595
600
Leu Ile Pro Asp Val Gln Ala Pro Gly Leu Leu Val Met

5

————— Val ———— His

————— 605 ————— 610

————— 615

Glu ——— Leu ——— Pro ——— Ala ——— Gly ——— Lys ——— Gly ——— Val ——— Gln ——— Leu ——— Thr ——— Ala ——— Leu
————— Asn ——— Phe

————— 620 ————— 625

————— 630

Ser ——— Ala ——— Glu ——— Pro ——— Val ——— Ser ——— Glu ——— Thr ——— Ile ——— Cys ——— Leu ——— Pro ——— Gly
————— Val ——— Ala

————— 635 ————— 640

————— 645

Pro ——— Gly ——— Pro ——— Val ——— Val ——— Asp ——— Ile ——— Ile ——— His ——— Glu ——— Ser ——— Val ——— Glu
————— Gly ——— Asp

————— 650 ————— 655

————— 660

Leu ——— Thr ——— Asp ——— Asn ——— Cys ——— Glu ——— Leu ——— Gln ——— Ile ——— Asn ——— Leu ——— Asp ——— Pro
————— Tyr ——— Glu

————— 665 ————— 670

————— 675

Gly ——— Leu ——— Ala ——— Leu ——— Arg ——— Val ——— Val ——— Ser ——— Ala ——— Ala ——— Pro ——— Pro ——— Val
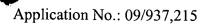————— Ile

————— 680 ————— 685.

2. (Currently Amended) An isolated trehalose synthase gene comprising the nucleotide

sequence as recited in SEQ ID NO: 1 with the following nucleotide sequence:

```
GATCGCTGGC GTACTGCAGG TAGAGCAGGC GCATCGGCCC CCAGGGCGCA TCGGCCGGCT   60
CCGCTGTGCC CTGCTGGTTC ATGAAGCGGA CGAAGCGGCC ATCGCGGAAC CGTGGACGCC   120
ATTCGGGGCT GTCCGGGTCG CGGCTGTCGG TGAGCGTGCG CCACAGGTCG CTGCGAAACG   180
GCGGACCGCT CCAAAGCGCG CCGTGGATGG GATCGCCGAG CAGTTCGTGC AGCTCCCAGG   240
AACGTTGCGA ATGCAGCGCG CCGAGGCTCA GGCCATGCAG ATACAGGCGC GGTCGGCGTT   300
CGGCCGGCAG TTCGGTCCAG TAGCCATAGA TCTCGGCGAA TAGCGCGCGG GCCACGTCGC   360
GGCCGTAGTC GGCCTCCACC AGCAGCGCCA GCGGGCTGTT CAGATAGGAG TACTGCAACG   420
CCACGCTGGC GATATCGCCG TGGTGCAGGT ATTCCACTGC GTTCATCGCC GCCGGGTCGA   480
TCCAGCCGGT ACCGGTGGGC GTCACCAGCA CCAGCACCGA TCGCTCGAAG GCGCCGCTGC   540
GCTGCAGCTC GCGCAAGGCC AGACGCGCCC GCTGGCGCGG GGTCTCTGCC GCGCGCAGAC   600
CGACGTAGAC GCGAATCGGC TCGAGCGCCG AGCGGCCGCT CAAGACGCTG ATATCCGCCG   660
CCGACGGGCC GGAGCCGATG AACTCGCGGC CGGTGCGGCC CAGCTCCTCC CAGCGCAGCA   720
ACGAGGCCCG GCTGCCGCTT TTCAGCGGCG AGGCCGGTGG CGCCGTCTCC GGTTCGATCA   780
GGGCGTCGTA CTGCGCGAAG GATGCGTCCA GCATGCGCAG TGCCCGCGCC GCCAGCACAT   840
CGCTGAGCAG CGACCAGAAC AGCGCCAGCG CCACCAGCAC GCCGATCACG TTGGCCAGGC   900
GCCGTGGCAG CACGCGGTCG GCGTGCCGCG AGACGAAGCG CGACACCAGC CGATACAGAC   960
GCGCCAGCGT CAGCAGGATG AGAAAGGTCG CCAGCGCGGT GAGAATGACT TCGAGCAGGT   1020
GCGCACTGCT CACCGGCGGC ATGCCCATCA CGCGTTCTGC CAGCCGGCGA   1080
CCTGGCTGAG GAAATACCCG GCCAGCAGCA GGCAGCCGAC CGCGATCAGC AGATTGACCC   1140
GCTCGCGCTG CCAGCCTGGG CGCTCCGGCA GTTCCAGATA GCGCCACAGC CAGCGCCAGA   1200
ACACGCCGAG GCCATAGCCC ACCGCCAGCG CCGCGCCGGC CAGCACGCCC TGGCTCAGCG   1260
TCGAGCGCGG CAGCAGCGAT GGCGTCAGCG CCGCGCAGAA GAACAGCGTG CCCAGCAGCA   1320
GGCCGAAACC GGACAGCGAG CGCCAGATAT AGAGGACGGG CAGGTGCAGC ATGAAGATCT   1380
CCGCGGTCGG GTGACGGCGT CGCGCCTCGG CATATCGAGG CGTGTCCGGT CGTGCGGTTC   1440
CCGTGATGGT CCGCAGCAGG CCAATCCGAT GCAACGATGG CCGAGCGGCC GACTCAAACG   1500
TCTACATTTC CCTAGTGCTG CCGGAACCGA TCGCCG                              1536
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ATG AGC ATC CCA GAC AAC ACC TAT ATC GAA TGG CTG GTC AGC CAG TCC        1584
Met Ser Ile Pro Asp Asn Thr Tyr Ile Glu Trp Leu Val Ser Gln Ser

ATG CTG CAT GCG GCC CGC GAG CGG TCG CGT CAT TAC GCC GGC CAG GCG        1632
Met Leu His Ala Ala Arg Glu Arg Ser Arg His Tyr Ala Gly Gln Ala

CGT CTC TGG CAG CGG CCT TAT GCC CAG GCC CGC CCG CGC GAT GCC AGC        1680
Arg Leu Trp Gln Arg Pro Try Ala Gln Ala Arg Pro Arg Asp Ala Ser
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6

GCC ATC GCC TCG GTG TGG TTC ACC GCC TAT CCG GCG GCC ATC ATC ACG ———— 1728
Ala Ile Ala Ser Val Trp Phe Thr Ala Tyr Pro Ala Ala Ile Ile Thr

CCG GAA GGC GGC ACG GTA CTC GAG GCC CTC GGC GAC GAC CGC CTC TGG ———— 1776
Pro Glu Gly Gly Thr Val Leu Glu Ala Leu Gly Asp Asp Arg Leu Trp

AGT GCG CTC TCC GAA CTC GGC GTG CAG GGC ATC CAC AAC GGG CCG ATG ———— 1824
Ser Ala Leu Ser Glu Leu Gly Val Gln Gly Ile His Asn Gly Pro Met

AAG CGT TCC GGT GGC CTG CGC GGA CGC GAG TTC ACC CCG ACC ATC GAC ———— 1872
Lys Arg Ser Gly Gly Leu Arg Gly Arg Glu Phe Thr Pro Thr Ile Asp

GGC AAC TTC GAC CGC ATC AGC TTC GAT ATC GAC CCG AGC CTG GGG ACC ———— 1920
Gly Asn Phe Asp Arg Ile Ser Phe Asp Ile Asp Pro Ser Leu Gly Thr

GAG GAG CAG ATG CTG CAG CTC AGC CGG GTG GCC GCG GCG CAC AAC GCC ———— 1968
Glu Glu Gln Met Leu Gln Leu Ser Arg Val Ala Ala Ala His Asn Ala

ATC GTC ATC GAC GAC ATC GTG CCG GCA CAC ACC GGG AAG GGT GCC GAC ———— 2016
Ile Val Ile Asp Asp Ile Val Pro Ala His Thr Gly Lys Gly Ala Asp

TTC CGC CTC GCG GAA ATG GCC TAT GGC GAC TAC CCC GGG CTG TAC CAC ———— 2064
Phe Arg Leu Ala Glu Met Ala Tyr Gly Asp Tyr Pro Gly Leu Tyr His

ATG GTG GAA ATC CGC GAG GAG GAC TGG GAG CTG CTG CCC GAG GTG CCG ———— 2112
Met Val Glu Ile Arg Glu Glu Asp Trp Glu Leu Leu Pro Glu Val Pro

GCC GGG CGT GAT TCG GTC AAC CTG CTG CCG CCG GTG GTC GAC CGG CTC ———— 2160
Ala Gly Arg Asp Ser Val Asn Leu Leu Pro Pro Val Val Asp Arg Leu

AAG GAA AAG CAC TAC ATC GTC GGC CAG CTG CAG CGG GTG ATC TTC TTC ———— 2208
Lys Glu Lys His Tyr Ile Val Gly Gln Leu Gln Arg Val Ile Phe Phe

GAG CCG GGC ATC AAG GAC ACC GAC TGG AGC GTC ACC GGC GAG GTC ACC ———— 2256
Glu Pro Gly Ile Lys Asp Thr Asp Trp Ser Val Thr Gly Glu Val Thr

GGG GTC GAC GGC AAG GTG CGT CGC TGG GTC TAT CTG CAC TAC TTC AAG ———— 2304
Gly Val Asp Gly Lys Val Arg Arg Trp Val Tyr Leu His Tyr Phe Lys

GAG GGC CAG CCG TCG CTG AAC TGG CTC GAC CCG ACC TTC GCC GCG CAG ———— 2352
Glu Gly Gln Pro Ser Leu Asn Trp Leu Asp Pro Thr Phe Ala Ala Gln

CAG CTG ATC ATC GGC GAT GCG CTG CAC GCC ATC GAC GTC ACC GGC GCC ———— 2400
Gln Leu Ile Ile Gly Asp Ala Leu His Ala Ile Asp Val Thr Gly Ala

CGG GTG CTG CGC CTG GAC GCC AAC GGC TTC CTC GGC GTG GAA CGG CGC ———— 2448
Arg Val Leu Arg Leu Asp Ala Asn Gly Phe Leu Gly Val Glu Arg Arg

GCC GAG GGC ACG GCC TGG TCG GAG GGC CAC CCG CTG TCC GTC ACC GGC ———— 2496
Ala Glu Gly Thr Ala Trp Ser Glu Gly His Pro Leu Ser Val Thr Gly

AAC CAG CTG CTC GCC GGG GCG ATC CGC AAG GCC GGC GGC TTC AGC TTC ———— 2544
Asn Gln Leu Leu Ala Gly Ala Ile Arg Lys Ala Gly Gly Phe Ser Phe
CAG GAG CTG AAC CTG ACC ATC GAT GAC ATC GCC GCC ATG TCC CAC GGC ———— 2592
Gln Glu Leu Asn Leu Thr Ile Asp Asp Ile Ala Ala Met Ser His Gly

GGG GCC GAT CTG TCC TAC GAC TTC ATC ACC CGC CCG GCC TAT CAC CAT ———— 2640
Gly Ala Asp Leu Ser Tyr Asp Phe Ile Thr Arg Pro Ala Tyr His His

GCG TTG CTC ACC GGC GAT ACC GAA TTC CTG CGC ATG ATG CTG CGC GAA ———— 2688
Ala Leu Leu Thr Gly Asp Thr Glu Phe Leu Arg Met Met Leu Arg Glu

GTG CAC GCC TTC GGC ATC GAC CCG GCG TCA CTG ATC CAT GCG CTG CAG ———— 2736
Val His Ala Phe Gly Ile Asp Pro Ala Ser Leu Ile His Ala Leu Gln

7

Cont B2

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AAC CAT GAC GAG TTC ACC CTG GAG CTG GTG CAC TTC TGG ACG CTG CAC          2784
Asn His Asp Glu Leu Thr Leu Glu Leu Val His Phe Trp Thr Leu His

GCC TAC GAC CAT TAC CAC TAC AAG GGC CAG ACC CTG CCC GGC GGC CAC          2832
Ala Tyr Asp His Tyr His Tyr Lys Gly Gln Thr Leu Pro Gly Gly His

CTG CGC GAA CAT ATC CGC GAG GAA ATG TAC GAG CGG CTG ACC GGC GAA          2880
Leu Arg Glu His Ile Arg Glu Glu Met Tyr Glu Arg Leu Thr Gly Glu

CAC GCG CCG TAC AAC CTC AAG TTC GTC ACC AAC GGG GTG TCC TGC ACC          2928
His Ala Pro Tyr Asn Leu Lys Phe Val Thr Asn Gly Val Ser Cys Thr

ACC GCC AGC GTG ATC GCC GCG GCG CTT AAC ATC CGT GAT CTG GAC GCC          2976
Thr Ala Ser Val Ile Ala Ala Ala Leu Asn Ile Arg Asp Leu Asp Ala

ATC GGC CCG GCC GAG GTG GAG CAG ATC CAG CGT CTG CAT ATC CTG CTG          3024
Ile Gly Pro Ala Glu Val Glu Gln Ile Gln Arg Leu His Ile Leu Leu

GTG ATG TTC AAT GCC ATG CAG CCC GGC GTG TTC GCC CTC TCC GGC TGG          3072
Val Met Phe Asn Ala Met Gln Pro Gly Val Phe Ala Leu Ser Gly Trp

GAT CTG GTC GGC GCC CTG CCG CTG GCG CCC GAG CAG GTC GAG CAC CTG          3120
Asp Leu Val Gly Ala Leu Pro Leu Ala Pro Glu Gln Val Glu His Leu

ATG GGC GAT GGC GAT ACC CGC TGG ATC AAT CGC GGC GGC TAT GAC CTC          3168
Met Gly Asp Gly Asp Thr Arg Trp Ile Asn Arg Gly Gly Tyr Asp Leu

GCC GAT CTG GCG CCG GAG GCG TCG GTC TCC GCC GAA GGC CTG CCC AAG          3216
Ala Asp Leu Ala Pro Glu Ala Ser Val Ser Ala Glu Gly Leu Pro Lys

GCC CGC TCG CTG TAC GGC AGC CTG GCC GAG CAG CTG CAG CGG CCA GGC          3264
Ala Arg Ser Leu Tyr Gly Ser Leu Ala Glu Gln Leu Gln Arg Pro Gly

TCC TTC GCC TGC CAG CTC AAG CGC ATC CTC AGC GTG CGC CAG GCC TAC          3312
Ser Phe Ala Cys Gln Leu Lys Arg Ile Leu Ser Val Arg Gln Ala Tyr

GAC ATC GCT GCC AGC AAG CAG ATC CTG ATT CCG GAT GTG CAG GCG CCG          3360
Asp Ile Ala Ala Ser Lys Gln Ile Leu Ile Pro Asp Val Gln Ala Pro

GGA CTC CTG GTG ATG GTC CAC GAG CTG CCT GCC GGC AAG GGC GTG CAG          3408
Gly Leu Leu Val Met Val His Glu Leu Pro Ala Gly Lys Gly Val Gln

CTC ACG GCA CTG AAC TTC AGC GCC GAG CCG GTC AGC GAG ACC ATC TGC          3456
Leu Thr Ala Leu Asn Phe Ser Ala Glu Pro Val Ser Glu Thr Ile Cys

CTG CCC GGC GTG GCG CCC GGC CCG GTG GTG GAC ATC ATT CAC GAG AGT          3504
Leu Pro Gly Val Ala Pro Gly Pro Val Val Asp Ile Ile His Glu Ser

GTG GAG GGC GAC CTC ACC GAC AAC TGC GAG CTG CAG ATC AAC CTC GAC          3552
Val Glu Gly Asp Leu Thr Asp Asn Cys Glu Leu Gln Ile Asn Leu Asp

CCG TAC GAG GGG CTT GCC CTG CGT GTG GTG AGC GCC GCG CCG CCG GTG          3600
Pro Tyr Glu Gly Leu Ala Leu Arg Val Val Ser Ala Ala Pro Pro Val

ATC TGA GCGC
            3610
Ile

CCTCTTCGCG CGCCCCGGGT CCGCCGCTAT AGTGCGCAGC GCCTGGGGCG CGCATTGCCC          3670
TCGCCGTCGA GACCAGCCCG TGTCGTTCAC TTCGCTTTTC CGCCTTGCGC TGCTGCCGCT          3730
GGCGCTGCTT GCCGCACCCG TCTGGGCGCA GACCGCCTGC CCGCCCGGCC AGCAGCCGAT          3790
CTGCCTGAGC GGCAGCTGCC TCTGCGTGCC GGCCGCCGCC AGCGATCCAC AGGCGGTCTA          3850
CGACCGCGTC CAGCGTATGG CTACGCTGGC CCTGCAGAAC TGGATCCAGC AGTCGCGCGA          3910
CCGCCTGATG GCCGGCGGCG TCGAGCCGAT ACCGCTGCAC ATCCGCTCGC AGCTCGAGCC          3970
GTATTTCGAT CTTGCCGTGC TGGAGAGTGC GCGGTACCGC GTCGGCGACG AGGTGGTGCT          4030
GACTGCCGGC AACACCCTGC TGCGCAACCC GGACGTCAAT GCCGTGACCC TGATCGACGT          4090
CATCGTCTTC CGCCACGAGG AGGATGCCCG GGACAACGTC GCGCTCTGGG CCCATGAGCT          4150
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CAAGCACGTC GAGCAATATC TGGACTGGGG CGTCGCCGAG TTCGCCCGGC GCTATACGCA   4210
GGATTTCCGT GCCGTGGAGC GCCCGGCCTA TGCGCTGGAG CGTGAGGTGG AAGAGGCCCT   4270
GCGCGAGACG CAGACGCGGC GCTGAGCGAG CTGATCGGTG CTGCTGCCCG CACTGGG CTG   4330
AAGCCCACCA ATGACGCCGG CGAAAACGAA AAACCCCGCC GAGGCGGGGT TTCTGACGCG   4390
GGTTGTGCGG TCAGCTCAGA ACGCCGGGAC CACGGCGCCC TTGTACTTTT CCTCGATGAA   4450
CTGGCGTACT TGCTCGCTGT GCAGCGCGGC AGCCAGTTTC TGCATGGCAT CGCTGTCCTT   4510
GTTGTCCGGA CGGGCGACCA GAATGTTCAC GTATGGCGAG TCGCTGCCCT CGATCACCAG   4570
GGCGTCCTGG GTCGGGTTCA GCTTGGCTTC CAGCGCGTAG TTGGTGTTGA TCAGCGCCAG   4630
GTCGACCTGG GTCAGCACGC GCGGCAGAGT CGCGGCTTCC AGTTCGCGGA TCTTGATCTT   4690
CTTCGGGTTC TCGGCGATGT CTTCGGCGTG GCGGTGATGC CGGCGCCGTC CTTCAGACCG   4750
ATC   4753]

3.   (Original) A recombinant plasmid containing the trehalose synthase gene of claim 1.

4.   (Original) The recombinant plasmid according to claim 1 which is recombinant plasmid pCJ122.

5.   (Currently Amended) A transformed ~~E. coli~~ *E. coli* with the recombinant plasmid of claim 1.

6.   (Currently Amended) The ~~transformant~~ transformed *E. coli* according to claim 5 in which the recombinant plasmid is pCJ122.

7.   (Original) A process for producing trehalose which comprises reacting the trehalose synthase enzyme of claim 1 with maltose solution to obtain trehalose.

8.   (Currently Amended) A process for producing trehalose which comprises ~~crushing~~ lysing the transformed *E. coli* of claim 5, centrifuging the ~~crushed~~ lysed bacteria, and reacting the resulting supernatant with maltose solution to obtain trehalose.

9.   (Currently Amended) A ~~novel~~ microorganism *Pseudomonas stutzeri* CJ38 that produces trehalose ~~form~~ from maltose.